

## RAW SEQUENCE LISTING

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Application Serial Number: 10/525, 710  
Source: PCT  
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PCT

## RAW SEQUENCE LISTING

DATE: 03/08/2005

PATENT APPLICATION: US/10/525,710

TIME: 10:00:55

Input Set : A:\Final Sequence List - 13111-6-US.txt

Output Set: N:\CRF4\03082005\J525710.raw

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4 <110> APPLICANT: Kroger, Burkhard
5      Zelder, Oskar
6      Kolpprogge, Corinna
7      Schroder, Hartwig
8      Hafner, Stefan
10 <120> TITLE OF INVENTION: Method for Zymotic Production of Fine Chemicals Containing
11      Sulphur (metY)
13 <130> FILE REFERENCE: 13111-00006-US
C--> 15 <140> CURRENT APPLICATION NUMBER: US/10/525,710
C--> 15 <141> CURRENT FILING DATE: 2005-02-24
15 <150> PRIOR APPLICATION NUMBER: PCT/EP 2003/009453
16 <151> PRIOR FILING DATE: 2003-08-26
18 <150> PRIOR APPLICATION NUMBER: DE 102 39 082.7
19 <151> PRIOR FILING DATE: 2002-08-26
21 <160> NUMBER OF SEQ ID NOS: 79
23 <170> SOFTWARE: PatentIn version 3.3
26 <210> SEQ ID NO: 1
28 <211> LENGTH: 1317
30 <212> TYPE: DNA
32 <213> ORGANISM: Corynebacterium diphtheriae
36 <220> FEATURE:
38 <221> NAME/KEY: CDS
40 <222> LOCATION: (1)..(1317)
44 <400> SEQUENCE: 1
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47 1          5          10          15
49 act cgc tcc atc cac gca gga caa agc gtc gat agt gat acc agt gcc      96
50 Thr Arg Ser Ile His Ala Gly Gln Ser Val Asp Ser Asp Thr Ser Ala
51          20          25          30
53 cgc aac cta ccg att tac ctg aca tca tcg tac gtt ttt aat gac gcc      144
54 Arg Asn Leu Pro Ile Tyr Leu Thr Ser Ser Tyr Val Phe Asn Asp Ala
55          35          40          45
57 gaa cac gca gca aac cgc ttc aac ctt tcc gac gcc ggc ccg gtt tac      192
58 Glu His Ala Ala Asn Arg Phe Asn Leu Ser Asp Ala Gly Pro Val Tyr
59          50          55          60
61 tct cgc ctg acc aac cca act gtc gcg gca gtc gaa gaa cgc cta gcc      240
62 Ser Arg Leu Thr Asn Pro Thr Val Ala Ala Val Glu Glu Arg Leu Ala
63 65          70          75          80
65 aat ctt gaa ggt ggc gta cac gcc gta ctt ttc gct tcc gga atg gcc      288
66 Asn Leu Glu Gly Gly Val His Ala Val Leu Phe Ala Ser Gly Met Ala
67          85          90          95
69 gcc gaa acc gcc gca atc ctc aac atc gcc cgc gcg ggt tcc cac atc      336

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70 Ala Glu Thr Ala Ala Ile Leu Asn Ile Ala Arg Ala Gly Ser His Ile
71          100          105          110
73 gtg tcc agt cct cgc att tac ggc ggc acc gaa aca ctc ttt gcc gtc      384
74 Val Ser Ser Pro Arg Ile Tyr Gly Gly Thr Glu Thr Leu Phe Ala Val
75          115          120          125
77 aca ttg gca cgc ctg ggc atc gaa acc act ttc gta gaa aat cct gac      432
78 Thr Leu Ala Arg Leu Gly Ile Glu Thr Thr Phe Val Glu Asn Pro Asp
79          130          135          140
81 gac cca gcc tca tgg gag gct gca gtt caa gac aac acg gta gct ctc      480
82 Asp Pro Ala Ser Trp Glu Ala Ala Val Gln Asp Asn Thr Val Ala Leu
83 145          150          155          160
85 tac gga gaa acc ttc gct aat cca caa gca gac gtg ctt gat att ccc      528
86 Tyr Gly Glu Thr Phe Ala Asn Pro Gln Ala Asp Val Leu Asp Ile Pro
87          165          170          175
89 gca atc gca gag gtt gcc cat aaa cat caa gta cca ctg atc gtc gac      576
90 Ala Ile Ala Glu Val Ala His Lys His Gln Val Pro Leu Ile Val Asp
91          180          185          190
93 aac acc ctc gca acc gca gcc ctt gta cgc ccc ctc gaa ctc ggt gca      624
94 Asn Thr Leu Ala Thr Ala Ala Leu Val Arg Pro Leu Glu Leu Gly Ala
95          195          200          205
97 gac gtc gtc gtg gca tcc cta acc aag ttc tac acc gga aat ggc tcc      672
98 Asp Val Val Val Ala Ser Leu Thr Lys Phe Tyr Thr Gly Asn Gly Ser
99          210          215          220
101 gga ctc ggc gga gtg ctt atc gac ggc gga aac ttc gac tgg acc gtc      720
102 Gly Leu Gly Gly Val Leu Ile Asp Gly Gly Asn Phe Asp Trp Thr Val
103 225          230          235          240
105 aca cgc aac ggc gaa ccg atc ttc ccc gac ttt gtc acc cca gat ccc      768
106 Thr Arg Asn Gly Glu Pro Ile Phe Pro Asp Phe Val Thr Pro Asp Pro
107          245          250          255
109 gcc tat cac ggt ctc aag tat tcc gat ctt ggt gcc ccc gcc ttc gga      816
110 Ala Tyr His Gly Leu Lys Tyr Ser Asp Leu Gly Ala Pro Ala Phe Gly
111          260          265          270
113 cta aag gct cgc gtc gga ctc ctg cgc gac acc ggc gca gcc cca tca      864
114 Leu Lys Ala Arg Val Gly Leu Leu Arg Asp Thr Gly Ala Ala Pro Ser
115          275          280          285
117 cca ctc aac gca tgg atc acc gca caa ggg ctc gac acc ctc tcg cta      912
118 Pro Leu Asn Ala Trp Ile Thr Ala Gln Gly Leu Asp Thr Leu Ser Leu
119          290          295          300
121 cga gta caa cgc cac aac gaa aac gca ctc gca gta gca caa ttc ctc      960
122 Arg Val Gln Arg His Asn Glu Asn Ala Leu Ala Val Ala Gln Phe Leu
123 305          310          315          320
125 gcc aac cac gag aaa gta gcc aag gtt aac tac gca ggc ctt ccc gac      1008
126 Ala Asn His Glu Lys Val Ala Lys Val Asn Tyr Ala Gly Leu Pro Asp
127          325          330          335
129 tcc cct tgg tac cca gtc aaa gaa aaa ctc gga ttc gac tac acc ggc      1056
130 Ser Pro Trp Tyr Pro Val Lys Glu Lys Leu Gly Phe Asp Tyr Thr Gly
131          340          345          350
133 tcc gta ctt tcc ttt gac gtt aaa ggt gga aaa aac gaa gca tgg cgc      1104
134 Ser Val Leu Ser Phe Asp Val Lys Gly Gly Lys Asn Glu Ala Trp Arg

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135          355          360          365
137 ttt atc gac gca ctc aaa cta cac tcg aac ctc gcc aac gtc gga gac      1152
138 Phe Ile Asp Ala Leu Lys Leu His Ser Asn Leu Ala Asn Val Gly Asp
139          370          375          380
141 gta cgt tcc ctc gta gtc cac cca gcg acc acc acg cac tca caa tcg      1200
142 Val Arg Ser Leu Val Val His Pro Ala Thr Thr Thr His Ser Gln Ser
143 385          390          395          400
145 gaa gaa tcg gca ctt cta gcc gca gga att aat caa gca acc atc cga      1248
146 Glu Glu Ser Ala Leu Leu Ala Ala Gly Ile Asn Gln Ala Thr Ile Arg
147          405          410          415
149 ctc tcc gtc ggc atc gaa tcc atc gac gac atc atc gcc gac ctc aca      1296
150 Leu Ser Val Gly Ile Glu Ser Ile Asp Asp Ile Ile Ala Asp Leu Thr
151          420          425          430
153 gca ggt ttc gac gca atc taa      1317
154 Ala Gly Phe Asp Ala Ile
155          435
158 <210> SEQ ID NO: 2
160 <211> LENGTH: 438
162 <212> TYPE: PRT
164 <213> ORGANISM: Corynebacterium diphtheriae
168 <400> SEQUENCE: 2
170 Met Pro Thr Lys Tyr Asp Asn Ser Asn Ala Asn Lys Trp Gly Phe Glu
171 1          5          10          15
174 Thr Arg Ser Ile His Ala Gly Gln Ser Val Asp Ser Asp Thr Ser Ala
175          20          25          30
178 Arg Asn Leu Pro Ile Tyr Leu Thr Ser Ser Tyr Val Phe Asn Asp Ala
179          35          40          45
182 Glu His Ala Ala Asn Arg Phe Asn Leu Ser Asp Ala Gly Pro Val Tyr
183          50          55          60
186 Ser Arg Leu Thr Asn Pro Thr Val Ala Ala Val Glu Glu Arg Leu Ala
187 65          70          75          80
190 Asn Leu Glu Gly Gly Val His Ala Val Leu Phe Ala Ser Gly Met Ala
191          85          90          95
194 Ala Glu Thr Ala Ala Ile Leu Asn Ile Ala Arg Ala Gly Ser His Ile
195          100          105          110
198 Val Ser Ser Pro Arg Ile Tyr Gly Gly Thr Glu Thr Leu Phe Ala Val
199          115          120          125
202 Thr Leu Ala Arg Leu Gly Ile Glu Thr Thr Phe Val Glu Asn Pro Asp
203          130          135          140
206 Asp Pro Ala Ser Trp Glu Ala Ala Val Gln Asp Asn Thr Val Ala Leu
207 145          150          155          160
210 Tyr Gly Glu Thr Phe Ala Asn Pro Gln Ala Asp Val Leu Asp Ile Pro
211          165          170          175
214 Ala Ile Ala Glu Val Ala His Lys His Gln Val Pro Leu Ile Val Asp
215          180          185          190
218 Asn Thr Leu Ala Thr Ala Ala Leu Val Arg Pro Leu Glu Leu Gly Ala
219          195          200          205
222 Asp Val Val Val Ala Ser Leu Thr Lys Phe Tyr Thr Gly Asn Gly Ser
223          210          215          220

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226 Gly Leu Gly Gly Val Leu Ile Asp Gly Gly Asn Phe Asp Trp Thr Val
227 225          230          235          240
230 Thr Arg Asn Gly Glu Pro Ile Phe Pro Asp Phe Val Thr Pro Asp Pro
231          245          250          255
234 Ala Tyr His Gly Leu Lys Tyr Ser Asp Leu Gly Ala Pro Ala Phe Gly
235          260          265          270
238 Leu Lys Ala Arg Val Gly Leu Leu Arg Asp Thr Gly Ala Ala Pro Ser
239          275          280          285
242 Pro Leu Asn Ala Trp Ile Thr Ala Gln Gly Leu Asp Thr Leu Ser Leu
243          290          295          300
246 Arg Val Gln Arg His Asn Glu Asn Ala Leu Ala Val Ala Gln Phe Leu
247 305          310          315          320
250 Ala Asn His Glu Lys Val Ala Lys Val Asn Tyr Ala Gly Leu Pro Asp
251          325          330          335
254 Ser Pro Trp Tyr Pro Val Lys Glu Lys Leu Gly Phe Asp Tyr Thr Gly
255          340          345          350
258 Ser Val Leu Ser Phe Asp Val Lys Gly Gly Lys Asn Glu Ala Trp Arg
259          355          360          365
262 Phe Ile Asp Ala Leu Lys Leu His Ser Asn Leu Ala Asn Val Gly Asp
263          370          375          380
266 Val Arg Ser Leu Val Val His Pro Ala Thr Thr Thr His Ser Gln Ser
267 385          390          395          400
270 Glu Glu Ser Ala Leu Leu Ala Ala Gly Ile Asn Gln Ala Thr Ile Arg
271          405          410          415
275 Leu Ser Val Gly Ile Glu Ser Ile Asp Asp Ile Ile Ala Asp Leu Thr
276          420          425          430
279 Ala Gly Phe Asp Ala Ile
280          435
283 <210> SEQ ID NO: 3
285 <211> LENGTH: 1350
287 <212> TYPE: DNA
289 <213> ORGANISM: Mycobacterium tuberculosis
293 <220> FEATURE:
295 <221> NAME/KEY: CDS
297 <222> LOCATION: (1)..(1350)
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305 1          5          10          15
307 tcg ttc gaa acc aaa cag ata cac gct ggt cag cac cct gat ccg acc      96
308 Ser Phe Glu Thr Lys Gln Ile His Ala Gly Gln His Pro Asp Pro Thr
309          20          25          30
311 acc aac gcc cgg gct ctg ccg atc tat gcg acc acg tcg tac acc ttc      144
312 Thr Asn Ala Arg Ala Leu Pro Ile Tyr Ala Thr Thr Ser Tyr Thr Phe
313          35          40          45
315 gac gac acc gcg cac gcc gcc gcc ctg ttc gga ctg gaa att ccg ggc      192
316 Asp Asp Thr Ala His Ala Ala Leu Phe Gly Leu Glu Ile Pro Gly
317          50          55          60
319 aat atc tac acc cgg atc ggc aac ccc acc acc gac gtc gtc gag cag      240

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320	Asn	Ile	Tyr	Thr	Arg	Ile	Gly	Asn	Pro	Thr	Thr	Asp	Val	Val	Glu	Gln	
321	65					70					75				80		
323	cgc	atc	gcc	gcg	ctc	gag	ggc	ggt	gtg	gcc	gcg	ctg	ttc	ctg	tcg	tcg	288
324	Arg	Ile	Ala	Ala	Leu	Glu	Gly	Gly	Val	Ala	Ala	Leu	Phe	Leu	Ser	Ser	
325					85				90						95		
327	ggg	cag	gcc	gcg	gag	acg	ttc	gcc	atc	ttg	aac	ctg	gcc	ggc	gcg	ggc	336
328	Gly	Gln	Ala	Ala	Glu	Thr	Phe	Ala	Ile	Leu	Asn	Leu	Ala	Gly	Ala	Gly	
329				100					105					110			
331	gat	cac	atc	gtg	tcc	agc	ccg	cgc	ctg	tac	ggc	ggc	acc	tac	aac	ctg	384
332	Asp	His	Ile	Val	Ser	Ser	Pro	Arg	Leu	Tyr	Gly	Gly	Thr	Tyr	Asn	Leu	
333			115					120					125				
335	ttc	cac	tat	tcg	ctg	gcc	aag	ctc	ggc	atc	gag	gtc	agc	ttc	gtc	gac	432
336	Phe	His	Tyr	Ser	Leu	Ala	Lys	Leu	Gly	Ile	Glu	Val	Ser	Phe	Val	Asp	
337		130					135				140						
339	gat	ccg	gac	gat	ctg	gac	acc	tgg	cag	gcg	gcg	gta	cgg	ccc	aac	acc	480
340	Asp	Pro	Asp	Asp	Leu	Asp	Thr	Trp	Gln	Ala	Ala	Val	Arg	Pro	Asn	Thr	
341	145				150				155						160		
343	aag	gcg	ttc	ttc	gcc	gag	acc	atc	tcc	aac	ccg	cag	atc	gac	ctg	ctg	528
344	Lys	Ala	Phe	Phe	Ala	Glu	Thr	Ile	Ser	Asn	Pro	Gln	Ile	Asp	Leu	Leu	
345				165				170						175			
347	gac	acc	ccg	gcg	gtt	tcc	gag	gtc	gcc	cat	cgc	aac	ggg	gtg	ccg	ttg	576
348	Asp	Thr	Pro	Ala	Val	Ser	Glu	Val	Ala	His	Arg	Asn	Gly	Val	Pro	Leu	
349			180					185					190				
351	atc	gtc	gac	aac	acc	atc	gcc	acg	cca	tac	ctg	atc	caa	ccg	ttg	gcc	624
352	Ile	Val	Asp	Asn	Thr	Ile	Ala	Thr	Pro	Tyr	Leu	Ile	Gln	Pro	Leu	Ala	
353			195				200						205				
355	cag	ggc	gcc	gac	atc	gtc	gtg	cat	tcg	gcc	acc	aag	tac	ctg	ggc	ggg	672
356	Gln	Gly	Ala	Asp	Ile	Val	Val	His	Ser	Ala	Thr	Ly's	Tyr	Leu	Gly	Gly	
357		210				215					220						
359	cac	ggt	gcc	gcc	atc	gcg	ggt	gtg	atc	gtc	gac	ggc	ggc	aac	ttc	gat	720
360	His	Gly	Ala	Ala	Ile	Ala	Gly	Val	Ile	Val	Asp	Gly	Gly	Asn	Phe	Asp	
361	225				230				235					240			
363	tgg	acc	cag	ggc	cgc	ttc	ccc	ggc	ttc	acc	acc	ccc	gac	ccc	agc	tac	768
364	Trp	Thr	Gln	Gly	Arg	Phe	Pro	Gly	Phe	Thr	Thr	Pro	Asp	Pro	Ser	Tyr	
365				245				250						255			
367	cac	ggc	gtg	gtg	ttc	gcc	gag	ctg	ggt	cca	ccg	gcg	ttt	gcg	ctc	aaa	816
368	His	Gly	Val	Val	Phe	Ala	Glu	Leu	Gly	Pro	Pro	Ala	Phe	Ala	Leu	Lys	
369			260					265					270				
371	gct	cga	gtg	cag	ctg	ctc	cgt	gac	tac	ggc	tcg	gcg	gct	tcg	ccg	ttc	864
372	Ala	Arg	Val	Gln	Leu	Leu	Arg	Asp	Tyr	Gly	Ser	Ala	Ala	Ser	Pro	Phe	
373			275					280					285				
375	aac	gcg	ttc	ttg	gtg	gcg	cag	ggt	ctg	gaa	acg	ctg	agc	ctg	cgg	atc	912
376	Asn	Ala	Phe	Leu	Val	Ala	Gln	Gly	Leu	Glu	Thr	Leu	Ser	Leu	Arg	Ile	
377		290				295					300						
379	gag	cgg	cac	gtc	gcc	aac	gcg	cag	cgc	gtc	gcc	gag	ttc	ctg	gcc	gcc	960
380	Glu	Arg	His	Val	Ala	Asn	Ala	Gln	Arg	Val	Ala	Glu	Phe	Leu	Ala	Ala	
381	305				310				315					320			
383	cgc	gac	gac	gtg	ctt	tcg	gtc	aac	tat	gcg	ggg	ctg	ccc	tcc	tcg	ccc	1008
384	Arg	Asp	Asp	Val	Leu	Ser	Val	Asn	Tyr	Ala	Gly	Leu	Pro	Ser	Ser	Pro	

VERIFICATION SUMMARY

DATE: 03/08/2005

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TIME: 10:00:56

Input Set : A:\Final Sequence List - 13111-6-US.txt

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L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date